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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/512,581B

DATE: 02/10/2003

TIME: 15:10:37

Input Set : A:\seqlistcorrected3.txt

Output Set: N:\CRF4\02102003\I512581B.raw

21

3 <110> APPLICANT: Soto, Ana M.
 4 Sonnenschein, Carlos
 5 Geck, Peter
 6 Szelei, Jozsef
 8 <120> TITLE OF INVENTION: A NOVEL ANDROGEN-INDUCED SUPPRESSOR OF CELL
 9 PROLIFERATION AND USES THEREOF
 11 <130> FILE REFERENCE: MBI-008
 13 <140> CURRENT APPLICATION NUMBER: US 09/512,581B
 14 <141> CURRENT FILING DATE: 2000-02-24
 16 <150> PRIOR APPLICATION NUMBER: US 60/121,461
 17 <151> PRIOR FILING DATE: 1999-02-24
 19 <160> NUMBER OF SEQ ID NOS: 8
 21 <170> SOFTWARE: PatentIn Ver. 2.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 5271
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (66)..(4238)
 32 <400> SEQUENCE: 1
 33 ccggagagcc ccggagttagcg agtcggcaac ccggagggtt agaaatattt 60
 35 ctgtc atg gct cat tca aag act agg acc aat gat gga aaa att aca tat 110
 36 Met Ala His Ser Lys Thr Arg Thr Asn Asp Gly Lys Ile Thr Tyr
 37 1 5 10 15
 39 ccg cct ggg gtc aag gaa ata tca gat aaa ata tct aaa gag gag atg 158
 40 Pro Pro Gly Val Lys Glu Ile Ser Asp Lys Ile Ser Lys Glu Glu Met
 41 20 25 30
 43 gtg aga cga tta aag atg gtt gtg aaa act ttt atg gat atg gac cag 206
 44 Val Arg Arg Leu Lys Met Val Val Lys Thr Phe Met Asp Met Asp Gln
 45 35 40 45
 47 gac tct gaa gaa aag gag ctt tat tta aac cta gct tta cat ctt 254
 48 Asp Ser Glu Glu Lys Glu Leu Tyr Leu Asn Leu Ala Leu His Leu
 49 50 55 60
 51 gct tca gat ttt ttt ctc aag cat cct ggt aaa gat gtt cgc tta ctg 302
 52 Ala Ser Asp Phe Phe Leu Lys His Pro Gly Lys Asp Val Arg Leu Leu
 53 65 70 75
 55 gta gcc tgc tgc ctt gct gat att ttc agg att tat gct cct gaa gct 350
 56 Val Ala Cys Cys Leu Ala Asp Ile Phe Arg Ile Tyr Ala Pro Glu Ala
 57 80 85 90 95
 59 cct tac aca tcc cct gat aaa cta aag gat ata ttt atg ttt ata aca 398
 60 Pro Tyr Thr Ser Pro Asp Lys Leu Lys Asp Ile Phe Met Phe Ile Thr
 61 100 105 110

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63	aga cag ttg aag	ggg cta gag gat	aca aag	agc cca caa	ttc aat agg	446			
64	Arg Gln Leu	Lys Gly Leu	Glu Asp	Thr Lys Ser	Pro Gln Phe Asn	Arg			
65	115	120			125				
67	tat ttt tat	tta ctt gag aac	att gct tgg	gtc aag tca	tat aac ata	494			
68	Tyr Phe	Tyr Leu	Leu Glu	Asn Ile	Ala Trp Val	Lys Ser Tyr Asn	Ile		
69	130	135			140				
71	tgc ttt gag	tta gaa gat	agc aat gaa	att ttc acc	cag cta tac	aga	542		
72	Cys Phe	Glu Leu	Glu Asp	Ser Asn	Glu Ilé	Phe Thr Gln	Leu Tyr Arg		
73	145	150			155				
75	acc tta ttt	tca gtt ata	aac aat ggc	cac aat cag	aaa gtc	cat atg	590		
76	Thr Leu	Phe Ser	Val Ile	Asn Asn	Gly His	Asn Gln Lys	Val His Met		
77	160	165			170		175		
79	cac atg gta	gac ctt atg	agc tct att	att tgt gaa	ggt gat	aca gtg	638		
80	His Met	Val Asp	Leu Met	Ser Ser	Ile Ile	Cys Glu Gly	Asp Thr Val		
81	180	185			190				
83	tct cag gag	ctt ttg gat	acg gtt tta	gta aat ctg	gtc cct	gct cat	686		
84	Ser Gln	Glu Leu	Leu Asp	Thr Val	Leu Val	Asn Leu	Val Pro Ala His		
85	195	200			205				
87	aag aat tta	aac aag caa	gca tat	gat ttg	gca aag	gct tta	ctg aag	734	
88	Lys Asn	Leu Asn	Lys Gln	Ala Tyr	Asp Leu	Ala Lys	Ala Leu	Leu Lys	
89	210	215			220				
91	agg aca	gct caa	gct att	gag cca	tat att	acc act	ttt ttt	aat cag	782
92	Arg Thr	Ala Gln	Ala Ile	Glu Pro	Tyr Ile	Thr Thr	Phe Phe	Asn Gln	
93	225	230			235				
95	gtt .ctg	atg ctt	ggg aaa	aca tct	atc agc	gat ttg	tca gag	cat gtc	830
96	Val Leu	Met Leu	Gly Lys	Thr Ser	Ile Ser	Asp Leu	Ser Glu	His Val	
97	240	245			250		255		
99	ttt gac tta	att ttg gag	ctc tac aat	att gat	agt cat	ttg ctg	ctc	878	
100	Phe Asp	Leu Ile	Leu Glu	Leu Tyr	Asn Ile	Asp Ser	His Leu	Leu	
101	260	265			270				
103	tct gtt tta	ccc cag	ctt gaa	ttt aaa	tta aag	agc aat	gat aat	gag	926
104	Ser Val	Leu Pro	Gln Leu	Glu Phe	Lys Leu	Lys Ser	Asn Asp	Asn Glu	
105	275	280			285				
107	gag cgc cta	caa gtt	aaa cta	ctg gca	aaa atg	ttt ggg	gca aag	974	
108	Glu Arg	Leu Gln	Val Val	Lys Leu	Leu Ala	Lys Met	Phe Gly	Ala Lys	
109	290	295			300				
111	gat tca	gaa ttg	gct tct	caa aac	aag cca	ctt tgg	cag tgc	tac ttg	1022
112	Asp Ser	Glu Leu	Ala Ser	Gln Asn	Lys Pro	Leu Trp	Gln Cys	Tyr Leu	
113	305	310			315				
115	ggc agg ttt	aat gat	atc cat	gta cca	atc cgc	ctg gaa	tgt gtg	aaa	1070
116	Gly Arg	Phe Asn	Asp Ile	His Val	Pro Ile	Arg Leu	Glu Cys	Val Lys	
117	320	325			330		335		
119	ttt gct	agc cat	tgt ctc	atg aac	cat cct	gat tta	gca aaa	gac tta	1118
120	Phe Ala	Ser His	Cys Leu	Met Asn	His Pro	Asp Leu	Ala Lys	Asp Leu	
121	340	345			350				
123	aca gag	tat ctt	aaa gtg	agg tca	cat gac	cct gag	gaa gct	att aga	1166
124	Thr Glu	Tyr Leu	Lys Val	Arg Ser	His Asp	Pro Glu	Glu Ala	Ile Arg	
125	355	360			365				
127	cat gat	gtt att	gtg tca	ata gtt	aca gct	gct aaa	aag gat	att ctt	1214

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128	His	Asp	Val	Ile	Val	Ser	Ile	Val	Thr	Ala	Ala	Lys	Lys	Asp	Ile	Leu	
129		370			375							380					
131	ctg	gtc	aat	gat	cac	tta	ctt	aat	ttt	gtg	aga	gag	aga	aca	tta	gac	1262
132	Leu	Val	Asn	Asp	His	Leu	Leu	Asn	Phe	Val	Arg	Glu	Arg	Thr	Leu	Asp	
133					385				390			395					
135	aaa	cga	tgg	aga	gta	cgc	aaa	gaa	gcc	atg	atg	gga	ctt	gcc	caa	att	1310
136	Lys	Arg	Trp	Arg	Val	Arg	Lys	Glu	Ala	Met	Met	Gly	Leu	Ala	Gln	Ile	
137	400					405				410			415				
139	tat	aag	aaa	tat	gct	tta	cag	tca	gca	gct	gga	aaa	gat	gct	gca	aaa	1358
140	Tyr	Lys	Tyr	Ala	Leu	Gln	Ser	Ala	Ala	Gly	Lys	Asp	Ala	Ala	Lys		
141					420				425			430					
143	cag	ata	gca	tgg	atc	aaa	gac	aaa	ttg	cta	cat	ata	tat	tat	caa	aat	1406
144	Gln	Ile	Ala	Trp	Ile	Lys	Asp	Lys	Leu	Leu	His	Ile	Tyr	Tyr	Gln	Asn	
145					435				440			445					
147	agt	att	gat	gat	cga	cta	ctt	gtt	gaa	cgg	atc	ttt	gct	caa	tac	atg	1454
148	Ser	Ile	Asp	Asp	Arg	Leu	Leu	Val	Glu	Arg	Ile	Phe	Ala	Gln	Tyr	Met	
149					450				455			460					
151	gtt	cct	cac	aat	tta	gaa	act	aca	gaa	cgg	atg	aaa	tgc	tta	tat	tac	1502
152	Val	Pro	His	Asn	Leu	Glu	Thr	Thr	Glu	Arg	Met	Lys	Cys	Leu	Tyr	Tyr	
153					465				470			475					
155	ttg	tat	gcc	aca	ctg	gat	tta	aat	gct	gtg	aaa	gca	ttg	aat	gaa	atg	1550
156	Leu	Tyr	Ala	Thr	Leu	Asp	Leu	Asn	Ala	Val	Lys	Ala	Leu	Asn	Glu	Met	
157	480					485				490			495				
159	tgg	aaa	tgt	caa	aat	ctg	ctc	cga	cat	caa	gta	aag	gat	ttg	ctt	gac	1598
160	Trp	Lys	Cys	Gln	Asn	Leu	Leu	Arg	His	Gln	Val	Lys	Asp	Leu	Leu	Asp	
161					500				505			510					
163	ttg	att	aag	caa	ccc	aaa	aca	gat	gcc	agt	gtc	aag	gcc	ata	ttt	tca	1646
164	Leu	Ile	Lys	Gln	Pro	Lys	Thr	Asp	Ala	Ser	Val	Lys	Ala	Ile	Phe	Ser	
165					515				520			525					
167	aaa	gtg	atg	gtt	att	aca	aga	aat	tta	cct	gat	cct	ggt	aag	gct	cag	1694
168	Lys	Val	Met	Val	Ile	Thr	Arg	Asn	Leu	Pro	Asp	Pro	Gly	Lys	Ala	Gln	
169					530				535			540					
171	gat	ttc	atg	aag	aaa	ttc	aca	cag	gtg	tta	gaa	gat	gat	gag	aaa	ata	1742
172	Asp	Phe	Met	Lys	Lys	Phe	Thr	Gln	Val	Leu	Glu	Asp	Asp	Glu	Lys	Ile	
173					545				550			555					
175	aga	aag	cag	tta	gaa	gta	ctt	gtt	agt	cca	aca	tgc	tcc	tgc	aag	cag	1790
176	Arg	Lys	Gln	Leu	Glu	Val	Leu	Val	Ser	Pro	Thr	Cys	Ser	Cys	Lys	Gln	
177	560					565				570			575				
179	gct	gaa	ggt	tgt	gtg	cgt	gaa	ata	act	aag	aag	ttg	ggc	aac	ccc	aaa	1838
180	Ala	Glu	Gly	Cys	Val	Arg	Glu	Ile	Thr	Lys	Lys	Leu	Gly	Asn	Pro	Lys	
181					580				585			590					
183	cag	cct	aca	aat	cct	ttc	ctg	gaa	atg	atc	aag	ttt	ctc	ttg	gag	agg	1886
184	Gln	Pro	Thr	Asn	Pro	Phe	Leu	Glu	Met	Ile	Lys	Phe	Leu	Leu	Glu	Arg	
185					595				600			605					
187	ata	gca	cct	gtg	cac	ata	gat	acc	gaa	tct	atc	agt	gct	ttt	att	aaa	1934
188	Ile	Ala	Pro	Val	His	Ile	Asp	Thr	Glu	Ser	Ile	Ser	Ala	Leu	Ile	Lys	
189					610				615			620					
191	caa	gtg	aac	aaa	tca	ata	gat	gga	aca	gca	gat	gat	gaa	gat	gag	ggt	1982
192	Gln	Val	Asn	Lys	Ser	Ile	Asp	Gly	Thr	Ala	Asp	Asp	Glu	Asp	Glu	Gly	

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193	625	630	635	
195	gtt cca act gat caa gcc atc aga gca ggt ctt gaa ctg ctt aag gta	2030		
196	Val Pro Thr Asp Gln Ala Ile Arg Ala Gly Leu Glu Leu Leu Lys Val			
197	640	645	650	655
199	ctc tca ttt aca cat ccc atc tca ttt cat tct gct gaa aca ttt gaa	2078		
200	Leu Ser Phe Thr His Pro Ile Ser Phe His Ser Ala Glu Thr Phe Glu			
201	660	665	670	
203	tca tta ctg gct tgt ctg aaa atg gat gat gaa aaa gta gca gaa gct	2126		
204	Ser Leu Leu Ala Cys Leu Lys Met Asp Asp Glu Lys Val Ala Glu Ala			
205	675	680	685	
207	gca cta caa att ttc aaa aac aca gga agc aaa att gaa gag gat ttt	2174		
208	Ala Leu Gln Ile Phe Lys Asn Thr Gly Ser Lys Ile Glu Glu Asp Phe			
209	690	695	700	
211	cca cac atc aga tca gcc ttg ctt cct gtt tta cat cac aaa tct aaa	2222		
212	Pro His Ile Arg Ser Ala Leu Leu Pro Val Leu His His Lys Ser Lys			
213	705	710	715	
215	aaa gga ccc ccc cgt caa gcc aaa tat gcc att cat tgt atc cat gcg	2270		
216	Lys Gly Pro Pro Arg Gln Ala Lys Tyr Ala Ile His Cys Ile His Ala			
217	720	725	730	735
219	ata ttt tct agt aaa gag acc cag ttt gca cag ata ttt gag cct ctg	2318		
220	Ile Phe Ser Ser Lys Glu Thr Gln Phe Ala Gln Ile Phe Glu Pro Leu			
221	740	745	750	
223	cat aag agc cta gat cca agc aac ctg gaa cat ctc ata aca cca ttg	2366		
224	His Lys Ser Leu Asp Pro Ser Asn Leu Glu His Leu Ile Thr Pro Leu			
225	755	760	765	
227	gtt act att ggt cat att gct ctc ctt gca cct gat caa ttt gct gct	2414		
228	Val Thr Ile Gly His Ile Ala Leu Leu Ala Pro Asp Gln Phe Ala Ala			
229	770	775	780	
231	cct tgg aaa tct tgg gta gct act ttc att gtg aaa gat ctt ctc atg	2462		
232	Pro Trp Lys Ser Trp Val Ala Thr Phe Ile Val Lys Asp Leu Leu Met			
233	785	790	795	
235	aat gat cgg ctt cca ggg aaa aag aca act aaa ctt tgg gtt cca gat	2510		
236	Asn Asp Arg Leu Pro Gly Lys Lys Thr Thr Lys Leu Trp Val Pro Asp			
237	800	805	810	815
239	gaa gaa gta tct cct gag aca atg gtc aaa att cag gct att aaa atg	2558		
240	Glu Glu Val Ser Pro Glu Thr Met Val Lys Ile Gln Ala Ile Lys Met			
241	820	825	830	
243	atg gtt cga tgg cta ctt gga atg aaa aat aat cac agt aaa tca gga	2606		
244	Met Val Arg Trp Leu Leu Gly Met Lys Asn Asn His Ser Lys Ser Gly			
245	835	840	845	
247	act tct acc tta aga ttg cta aca aca ata ttg cat agt gat gga gac	2654		
248	Thr Ser Thr Leu Arg Leu Leu Thr Thr Ile Leu His Ser Asp Gly Asp			
249	850	855	860	
251	ttg aca gaa cag ggg aaa att agt aaa cca gat atg tca cgt ctg aga	2702		
252	Leu Thr Glu Gln Gly Lys Ile Ser Lys Pro Asp Met Ser Arg Leu Arg			
253	865	870	875	
255	ctt gct gct ggg agt gct att gtg aag ctg gca caa gaa ccc tgt tac	2750		
256	Leu Ala Ala Gly Ser Ala Ile Val Lys Leu Ala Gln Glu Pro Cys Tyr			
257	880	885	890	895

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259 cat gaa atc atc aca tta gaa caa tat cag cta tgt gca tta gct atc	2798
260 His Glu Ile Ile Thr Leu Glu Gln Tyr Gln Leu Cys Ala Leu Ala Ile	
261 900 905 910	
263 aac gat gaa tgc tat caa gta aga caa gtg ttt gcc cag aaa ctt cac	2846
264 Asn Asp Glu Cys Tyr Gln Val Arg Gln Val Phe Ala Gln Lys Leu His	
265 915 920 925	
267 aaa ggc ctt tcc cgt tta cgg ctt cca ctt gag tat atg gca atc tgt	2894
268 Lys Gly Leu Ser Arg Leu Arg Leu Pro Leu Glu Tyr Met Ala Ile Cys	
269 930 935 940	
271 gcc ctt tgt gca aaa gat cct gta aag gag aga aga gct cat gct agg	2942
272 Ala Leu Cys Ala Lys Asp Pro Val Lys Glu Arg Arg Ala His Ala Arg	
273 945 950 955	
275 caa tgt ttg gtg aaa aat ata aat gta agg cgg gag tat ctg aag cag	2990
276 Gln Cys Leu Val Lys Asn Ile Asn Val Arg Arg Glu Tyr Leu Lys Gln	
277 960 965 970 975	
279 cat gca gct gtt agt gaa aaa tta ttg tct ctt cta cca gag tat gtt	3038
280 His Ala Ala Val Ser Glu Lys Leu Leu Ser Leu Leu Pro Glu Tyr Val	
281 980 985 990	
283 gtt cca tat aca att cac ctt ttg gca cat gac cca gat tat gtc aaa	3086
284 Val Pro Tyr Thr Ile His Leu Leu Ala His Asp Pro Asp Tyr Val Lys	
285 995 1000 1005	
287 gta cag gat att gaa caa ctt aaa gat gtt aaa gaa tgt ctt tgg ttt	3134
288 Val Gln Asp Ile Glu Gln Leu Lys Asp Val Lys Glu Cys Leu Trp Phe	
289 1010 1015 1020	
291 gtt ctg gaa ata tta atg gct aaa aat gaa aat aac agt cac gct ttt	3182
292 Val Leu Glu Ile Leu Met Ala Lys Asn Glu Asn Asn Ser His Ala Phe	
293 1025 1030 1035	
295 atc aga aag atg gta gaa aat att aaa caa aca aaa gat gcc caa gga	3230
296 Ile Arg Lys Met Val Glu Asn Ile Lys Gln Thr Lys Asp Ala Gln Gly	
297 1040 1045 1050 1055	
299 cca gat gat gca aaa atg aat gaa aaa ctg tac act gtg tgt gat gtt	3278
300 Pro Asp Asp Ala Lys Met Asn Glu Lys Leu Tyr Thr Val Cys Asp Val	
301 1060 1065 1070	
303 gcc atg aat atc atc atg tca aag agt act aca tac agt ttg gaa tct	3326
304 Ala Met Asn Ile Ile Met Ser Lys Ser Thr Thr Tyr Ser Leu Glu Ser	
305 1075 1080 1085	
307 cct aaa gac ccg gta cta cca gct cgt ttc ttc act caa cct gac aag	3374
308 Pro Lys Asp Pro Val Leu Pro Ala Arg Phe Phe Thr Gln Pro Asp Lys	
309 1090 1095 1100	
311 aat ttc agt aac acc aaa aat tat ctg cct cct gaa atg aaa tca ttt	3422
312 Asn Phe Ser Asn Thr Lys Asn Tyr Leu Pro Pro Glu Met Lys Ser Phe	
313 1105 1110 1115	
315 ttc act cct gga aaa cct aaa aca acc aat gtt cta gga gct gtt aac	3470
316 Phe Thr Pro Gly Lys Pro Lys Thr Thr Asn Val Leu Gly Ala Val Asn	
317 1120 1125 1130 1135	
319 aag cca ctt tca tca gca ggc aag caa tct cag acc aaa tca tca cga	3518
320 Lys Pro Leu Ser Ser Ala Gly Lys Gln Ser Gln Thr Lys Ser Ser Arg	
321 1140 1145 1150	
323 atg gaa act gta agc aat gca agc agc agc tca aat cca agc tct cct	3566

RAW SEQUENCE LISTING ERROR SUMMARY
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Seq#:2; Line(s) 512,513,514,515,516,517,518,519,520,521,522,523,524,525,526
Seq#:2; Line(s) 527,528,529,530,531,532,533,534,535,536,537,538,539,540,541
Seq#:2; Line(s) 542,543,544,545,546,547,548,549,550,551,552,553,554,555,556
Seq#:2; Line(s) 557,558,559,560,561,562,563,564,565,566,567,568,569,570,571
Seq#:2; Line(s) 572,573,574,575,576,577,578,579,580,581,582,583,584,585,586
Seq#:2; Line(s) 587,588,589,590,591,592,593,594,595,596,597,598,599,600,601
Seq#:2; Line(s) 602,603,604,605,606,607,608,609,610,611,612,613,614,615,616
Seq#:2; Line(s) 617,618,619,620,621,622,623,624,625,626,627,628,629,630,631
Seq#:2; Line(s) 632,633,634,635,636,637,638,639,640,641,642,643,644,645,646
Seq#:2; Line(s) 647,648,649,650,651,652,653,654,655,656,657,658,659,660,661
Seq#:2; Line(s) 662,663,664,665,666,667,668,669,670,671,672,673,674,675,676

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 02/10/2003
PATENT APPLICATION: US/09/512,581B TIME: 15:10:38

Input Set : A:\seqlistcorrected3.txt
Output Set: N:\CRF4\02102003\I512581B.raw

Seq#:2; Line(s) 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689
Seq#:3; Line(s) 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704
Seq#:3; Line(s) 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719
Seq#:3; Line(s) 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734
Seq#:3; Line(s) 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749
Seq#:3; Line(s) 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764
Seq#:3; Line(s) 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779
Seq#:3; Line(s) 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794

VERIFICATION SUMMARY

PATENT APPLICATION: **US/09/512,581B**

DATE: 02/10/2003

TIME: 15:10:38

Input Set : **A:\seqlistcorrected3.txt**
Output Set: **N:\CRF4\02102003\I512581B.raw**

L:1838 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7